

Sequence Listing

- <110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
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<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu	1	5	10	15
Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys	20	25	30	
Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala	35	40	45	
Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys	50	55	60	
Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu	65	70	75	
Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val	80	85	90	
Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly	95	100	105	
Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala	110	115	120	
Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu	125	130	135	
Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro	140	145	150	
Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val	155	160	165	
Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys	170	175	180	
Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys	185	190	195	

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315

Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctggt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggcggg 100
 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcgggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagtgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaattc acccgcttta ccagctctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
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cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
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ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
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 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500
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 ttgatttgc ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

[illegible]

395					400					405						
Arg	Glu	Leu	Ser	410	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala	420
Val	Glu	Lys	Val	425	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys	435
Asp	Gly	Leu	Val	440	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe	450
Thr	His	Leu	Gly	455	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr	465
Tyr	Glu	Tyr	Leu	470	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu	480
Thr	Gln	Leu	Leu	485	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg	495
Thr	His	Leu	Leu	500	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val	510
Gly	Glu	Leu	Ala	515	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu	525
Val	Cys	Phe	Leu	530	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly	540
Leu	Pro	Ala	Ser	545	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr	555
Cys	Tyr	Gln	Met	560	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu	570
Ile	Val	His	Phe	575	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val	585
Glu	Val	Lys	Pro	590	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr	600
Val	Glu	Ser	Leu	605	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys	615
Tyr	Gln	Asp	Trp	620	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe	630
Thr	Arg	Val	Pro	635	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln	645
Asp	Pro	Gln	Lys	650	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe	660
Leu	Gly	Glu	Thr	665	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp	675
Pro	Asn	Leu	Leu	680	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala	690

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 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
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 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
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 acaggagcag ttcaaggtgg acaggaggagg aggcctgaac actgtgaagt 950
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 ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
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 cgggaccccc cctgccttcc tgctcacctt actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

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<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1             5             10             15
Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
             20             25             30
Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
             35             40             45
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
             50             55             60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
             65             70             75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
             80             85             90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
             95             100             105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
             110             115             120
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
             125             130             135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

```

	140		145		150
Glu Ser Ser Asn	Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp			
	155	160			165
Leu Leu Pro Leu	Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala			
	170	175			180
Gly Pro Phe His	Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His			
	185	190			195
Tyr Lys Thr Tyr	Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His			
	200	205			210
Tyr Arg Leu Cys	Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly			
	215	220			225
Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu			
	230	235			240
Gln Leu Phe Arg	Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe			
	245	250			255
Arg His Leu His	Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg			
	260	265			270
Ile Ala Ala Gln	Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly			
	275	280			285
Gly Leu Asn Thr	Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu			
	290	295			300
Ser Val Gly Gly	Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp			
	305	310			315
Cys Asp Lys Thr	Ala Thr Pro Trp Cys	Thr Phe Ser			
	320	325			

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
 <223> Synthetic construct

<400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 21
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 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
 gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
 tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250
 gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300
 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
 atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
 cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 3-18

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 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat ttataactg cagtgggtata aatgcaaata tactattgtt 2300

acatgtgaaa	aaatttttatt	tgacttaaaa	gtttattttat	ttgtttttttt	2350
gctcctgatt	ttaagacaat	aagatgtttt	catgggcccc	taaaagtatc	2400
atgagccttt	ggcactgcg	ctgccaaagc	tagtggagaa	gtcaaccctg	2450
agaccaggtg	tttaatcaag	caagctgtat	atcaaaaattt	ttggcagaaa	2500
acacaaatat	gtcatatatc	ttttttttaa	aaaagtattt	cattgaagca	2550
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atttgactac	actgtattga	agcaaataga	ggaggcacaa	ctccagcacc	2650
ctaattggaac	cacatttttt	tacttagct	ttctgtgggc	atgtgtaatt	2700
gtattctctg	cggtttttta	tctcacagta	ctttattttct	gtcttgtccc	2750
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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens
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<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.
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<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).
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<400> 24  
Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu  
   1           5          10         15  
  
Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
      20                25        30  
  
Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
      35              40       45  
  
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
      50            55        60  
  
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
      65            70       75  
  
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
      80            85       90
```

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380										385					390				
Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe					
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
				425					430					435					
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
				440					445					450					
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu					
				455					460					465					
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
				470					475					480					
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
				485					490					495					
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala					
				500					505					510					
Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
				515					520					525					
Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile					
				530					535					540					
Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met					
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly					
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Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
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Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
				590					595					600					
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- <211> 24
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttgggagaac agattatctt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300

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tgtccagtgc ttaggggtgt tactgagaag cactgccgag cttgtgagaa 550

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gtggagggag agacgctcct gatcgctgaa tcc 683

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<211> 81

<212> PRT

<213> Homo sapiens

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<221> sig_peptide

<222> 1-21

<223> Signal peptide.

<400> 29

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75

Lys Gly Ser Gln Lys Ser
80

<210> 30

<211> 2128

<212> DNA

<213> Homo sapiens

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tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150

caccaccatc acaaccacca cgacgtcatc ttctgggctg gggcccccca 200

tgatcggtgg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250

ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgctgg tggttagcgt 300

gggcgcctgg acgggggtcca tgggcaactg gtccatgttc acctgggtgct 350

tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400

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 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
215 220 225
Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
245 250 255
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
275 280 285
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
290 295 300
Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
305 310 315
His Leu Val Phe Val Lys Val
320

<210> 32
<211> 3680
<212> DNA
<213> Homo sapiens

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ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
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<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33
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20 25 30
Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45
His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60
Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75
Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90
Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105
Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120
Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

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<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
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<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
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<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
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gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
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ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phè	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgacg tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
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ttccgccttc gtgcgagaga cctcttgctg ggtttcaaca aacgtgccat 800
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tcaagatatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
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ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
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aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
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ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

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 ccgagcctcc cgccaccctg gaccccggcc ctccagccca catcgatggg 350
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 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
 ggctccctgg cttttctgct gatgttcatc gtctgtgccg cggtcacac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgtec ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
 cccccaccag ggctgcaactg ggcgggtggg acggagccag gatggtggag 750
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 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
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 tccttcacct cagcagcccc aaagggtac atctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
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 aatactgctc ttaattttcc tgaagggtgg ccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
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agaagctgag gggctgtggt tgaggggacc tccaccctgg ggaagtccga 1650
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ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
aaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
1 5 10 15
Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caaactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaaggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
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 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtccctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
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 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

				50						55				60
Gly	Ala	Ala	Gly	Ser 65	Lys	Val	Ser	Glu	Ala 70	Leu	Gly	Gln	Gly	Thr 75
Arg	Glu	Ala	Val	Gly 80	Thr	Gly	Val	Arg	Gln 85	Val	Pro	Gly	Phe	Gly 90
Ala	Ala	Asp	Ala	Leu 95	Gly	Asn	Arg	Val	Gly 100	Glu	Ala	Ala	His	Ala 105
Leu	Gly	Asn	Thr	Gly 110	His	Glu	Ile	Gly	Arg 115	Gln	Ala	Glu	Asp	Val 120
Ile	Arg	His	Gly	Ala 125	Asp	Ala	Val	Arg	Gly 130	Ser	Trp	Gln	Gly	Val 135
Pro	Gly	His	Ser	Gly 140	Ala	Trp	Glu	Thr	Ser 145	Gly	Gly	His	Gly	Ile 150
Phe	Gly	Ser	Gln	Gly 155	Gly	Leu	Gly	Gly	Gln 160	Gly	Gln	Gly	Asn	Pro 165
Gly	Gly	Leu	Gly	Thr 170	Pro	Trp	Val	His	Gly 175	Tyr	Pro	Gly	Asn	Ser 180
Ala	Gly	Ser	Phe	Gly 185	Met	Asn	Pro	Gln	Gly 190	Ala	Pro	Trp	Gly	Gln 195
Gly	Gly	Asn	Gly	Gly 200	Pro	Pro	Asn	Phe	Gly 205	Thr	Asn	Thr	Gln	Gly 210
Ala	Val	Ala	Gln	Pro 215	Gly	Tyr	Gly	Ser	Val 220	Arg	Ala	Ser	Asn	Gln 225
Asn	Glu	Gly	Cys	Thr 230	Asn	Pro	Pro	Pro	Ser 235	Gly	Ser	Gly	Gly	Gly 240
Ser	Ser	Asn	Ser	Gly 245	Gly	Gly	Ser	Gly	Ser 250	Gln	Ser	Gly	Ser	Ser 255
Gly	Ser	Gly	Ser	Asn 260	Gly	Asp	Asn	Asn	Asn 265	Gly	Ser	Ser	Ser	Gly 270
Gly	Ser	Ser	Ser	Gly 275	Ser	Ser	Ser	Gly	Ser 280	Ser	Ser	Gly	Gly	Ser 285
Ser	Gly	Gly	Ser	Ser 290	Gly	Gly	Ser	Ser	Gly 295	Asn	Ser	Gly	Gly	Ser 300
Arg	Gly	Asp	Ser	Gly 305	Ser	Glu	Ser	Ser	Trp 310	Gly	Ser	Ser	Thr	Gly 315
Ser	Ser	Ser	Gly	Asn 320	His	Gly	Gly	Ser	Gly 325	Gly	Gly	Asn	Gly	His 330
Lys	Pro	Gly	Cys	Glu 335	Lys	Pro	Gly	Asn	Glu 340	Ala	Arg	Gly	Ser	Gly 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435
Ser Ser Arg Ile Pro
440

<210> 53
<211> 3580
<212> DNA
<213> Homo sapiens

<400> 53
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ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
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cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
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ggccggtaga caaagtggaa gtcgcgcttg ggctcgtgc gcagcaggta 3500
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cgtccaccag cacgaacagc cgggtgcgct 3580

<210> 54
<211> 280
<212> PRT
<213> Homo sapiens

<400> 54
Met Cys Phe Leu Asn Lys Leu Leu Leu Leu Ala Val Leu Gly Trp
1 5 10 15
Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu
20 25 30
Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
35 40 45
His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
50 55 60
Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
65 70 75
Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
80 85 90
Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
95 100 105
Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
110 115 120
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Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
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Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
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Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
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Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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 <212> DNA
 <213> Homo sapiens

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<210> 56
 <211> 299
 <212> PRT
 <213> Homo sapiens

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<211> 4277
<212> DNA
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 <211> 1115

<212> PRT
<213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
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Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

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 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
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 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
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His	Gly	Arg	Leu	Ser 605	Pro	Pro	Glu	Ala		Pro 610	Asp	Arg	Pro	Thr	Ile 615
Ser	Thr	Ala	Ser	Glu 620	Thr	Ser	Val	Tyr		Val 625	Thr	Trp	Ile	Pro	Arg 630
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Pro	Pro	Ser	Arg	Leu 665	Ser	Val	Glu	Ile		Thr 670	Gly	Leu	Glu	Lys	Gly 675
Thr	Ser	Tyr	Lys	Phe 680	Arg	Val	Arg	Ala		Leu 685	Asn	Met	Leu	Gly	Glu 690
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Lys	Ala	Arg	Lys	Ser 815	Ser	Gly	Gln	Pro		Gly 820	Arg	Leu	Pro	Pro	Pro 825
Thr	Leu	Ala	Pro	Pro 830	Gln	Pro	Pro	Leu		Pro 835	Glu	Thr	Ile	Glu	Arg 840
Pro	Val	Gly	Thr	Gly 845	Ala	Met	Val	Ala		Arg 850	Ser	Ser	Asp	Leu	Pro 855

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<212> DNA
<213> Artificial
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 <223> Synthetic construct.

<400> 59
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<210> 60
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 60
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<210> 61
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 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

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 <223> unknown base

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<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 65
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<210> 66
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
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<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
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 aacacccaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100
 ggcccagcaa gcctgataag catgaagctc ttatcttttg tggtgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
 gcccatgcca gtgcctggcc atgacgtgga ggctactgc ctgctgtgcg 350
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
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ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
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Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
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Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
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tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggctctccc 150
tccctttgca ttcccacccc tccgggcttt gcgtcttctt ggggaccccc 200
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tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
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gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
gcatgtgctg cccagttacc cgctgcaata atggcatctg tatcccagtt 600
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 atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
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 gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900
 tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
 ctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
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 gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
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 caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
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 aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaaatt 1450
 gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
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aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

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<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens
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<400> 71
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acatcacggtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttcccttta acttcttatg tcagaatgag gaagggatagc tqcatttatt 200
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tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
atatttttagt aattcatatg ttttagatta taggttttaa catacttggtg 300
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattggtga 350
ggatttggtc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatcccc gtccctcagtc ctcagtcctc ttgacttcaa 600
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aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050
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Ser Ser Glu Asn	Ser Asn Gln Ile Pro	Ile Ser Leu Tyr Ser	Lys
230		235	240
Ser Leu Ser Glu	Pro Leu Asn Thr Ser	Leu Ser Met Thr Ser	Ala
245		250	255
Val Gln Asn Ser	Thr Tyr Thr Thr Ser	Val Ile Thr Ser Cys	Ser
260		265	270
Leu Thr Ser Ser	Ser Leu Asn Ser Ala	Ser Pro Val Ala Met	Ser
275		280	285
Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr	Gln
290		295	300
Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met	Asn
305		310	315
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys	Tyr
320		325	330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln	Arg
335		340	345
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Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
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<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
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<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
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gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

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<210> 77
 <211> 341
 <212> PRT
 <213> Homo sapiens

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<400> 77
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          20             25             30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
          35             40             45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
          50             55             60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
          65             70             75

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Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
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Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
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Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
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Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
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Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
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Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
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Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
230 235 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
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Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
260 265 270

Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
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Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
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Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
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Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
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Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
335 340 345

Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
350 355 360

Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
365 370 375

Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
380 385 390

Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

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395                               400                               405
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Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
425                               430                               435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
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<212> DNA

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<212> PRT
<213> Homo sapiens
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Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
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Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
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Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
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Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
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Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
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His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
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Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
				140					145					150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
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Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

	455		460		465
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly			
	470		475		480
Glu His Thr Ala	Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys			
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Ser Ala Leu Arg	Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro			
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Ala Ser Asp Thr	Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu			
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Gly Gln Gly His	Val His Gly Val Ala	Ser Ser Pro Ser His Asp			
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Leu Ala Lys Glu	Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu			
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 <212> DNA
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<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Leu	Pro	Leu	Ala	His 365	Met	Phe	Glu	Arg	Ile 370	Val	Gln	Ala	Val	Val 375
Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe 385	Gln	Gly	Asp	Ile	Arg 390
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Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
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Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
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Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
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His Ile Gln Asp

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 <213> Homo sapiens

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 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

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Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
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Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
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<210> 89
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 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-25
 <223> Synthetic construct.

 <400> 89

<400> 94

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 <211> 307
 <212> PRT
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 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Tyr	Val	Ala	Thr	Val 260	His	Val	Leu	Pro	Glu 265	Val	Gly	Gly	Ile	Gly 270	
His	Ser	His	Lys	Pro 275	Asp	Ala	Thr	Gly	Gly 280	Arg	Gly	Leu	Ser	Arg 285	
Leu	Glu	Val	Ala	Ala 290	Leu	Val	Leu	Gly	Cys 295	Leu	Ile	Pro	Leu	Ile 300	
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<210>	96
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<212>	DNA
<213>	Artificial

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<223> Synthetic construct.
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<211> 25
<212> DNA
<213> Artificial
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<220>
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<223> Synthetic construct.

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<211> 50
<212> DNA
<213> Artificial
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<222> 1-50
<223> Synthetic construct.
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<210> 99
<211> 1429
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<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctggtggcc tgcatcatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
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gagctgaaga agaacgagtt ccaggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
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aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatattt acaacagggc 1350

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$\langle 210 \rangle$ 100

<211> 401

<212> PRT

<213> Homo sapiens

$\langle 400 \rangle$ 100

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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

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Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
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Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	
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Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	
260	265 270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	
275	280 285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	
290	295 300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	
305	310 315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	
320	325 330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	
335	340 345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	
350	355 360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	
365	370 375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	
380	385 390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	
395	400

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 <212> DNA
 <213> Homo sapiens

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 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
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gcttttgtga tgagagtgga tgggtgctgt agctcctgg ttaggcagct 3250
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<210> 102

<211> 1089

<212> PRT

<213> Homo-sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	1	5	10	15
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785					790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly
				800					805					810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala
				815					820					825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu
				830					835					840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile
				845					850					855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu
				860					865					870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe
				875					880					885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr
				890					895					900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile
				905					910					915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser
				920					925					930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala
				935					940					945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp
				950					955					960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro
				965					970					975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu
				980					985					990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe
				995					1000					1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu
				1010					1015					1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025					1030					1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
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gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
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<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
170 175 180

Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
185 190 195

Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
200 205 210

Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
215 220 225

Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
230 235 240

Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
245 250 255

Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
260 265 270

Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
275 280 285

Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
290 295 300

Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
305 310 315

Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
320 325 330

Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
335 340 345

Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
350 355 360

Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
365 370 375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435

Leu Tyr Val Gln Met Glu Asn
440

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgcagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtagaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgttcggg ggccaacatc actgcggagg 250

cttctgctg cgagcccgtt ggggtggtct ggccgcccac tgcttcagcc 300

acagagacct ccgcaactgg ctggtggtgc tggcgccca cgtcctgagt 350

actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccagca 400

ccccgactac caccatga cccacgcaa cgacatctgc ctgctgoggc 450

tgaacggctc tgctgtctg ggcctgcag tggggctgct gaggtgcca 500

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cccgacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850

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tggtcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050

tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgtctc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgcccgtgt gctcaaggac 150
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacagggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggtctc cctcaagtct atccgagagt 400
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 aacgcgggtg tgatgcgggtg cccccactgg accaccgagg acggcttcga 500
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 ggaggetttg ggctgaaagt gcccgctgg tgggcttaga ggctccctct 1050
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 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
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 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

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<210> 118
<211> 544
<212> PRT
<213> Homo sapiens

<400> 118
Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
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Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr
20 25 30
Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45
Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60
Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75
His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90
Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105
Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120
Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135
Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150
Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165
Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180
Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

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Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens


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<400> 127
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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtccctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
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<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128
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Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens

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 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
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 aaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1 5 10 15
 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
110 115 120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
125 130 135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
155 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
185 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
215 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
245 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
260 265 270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
275 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
305 310 315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
320 325 330

Ser Phe Leu Met Ser
335

<210> 131
<211> 2476
<212> DNA
<213> Homo sapiens

<400> 131
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cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttggga 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
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agaatacaga caaagcagta aactggttaa gaaaggaagc aattaattac 700
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 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtggctcac 1850
 acctgtaatc ccaggacttt gggagggtga ggaaagcaga tcacaaggctc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagt tattttaaga taaaatgcc aatgattata 2200
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
 1 5 10 15
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcgat ctccctccctg 400
 gcctgcatta tctctgtggg gggcatgaga tgcacagtct tctgccagga 450

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atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatac 550
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
cagggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850
gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350
actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
gcagcctggg acatttaaaa aaata 1475

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<210> 134
<211> 230
<212> PRT
<213> Homo sapiens

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<400> 134
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
  1             5             10             15
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
             20             25             30
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
             35             40             45
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

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50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala	
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met	Val Thr Ser Ser Ala Ile	
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val	Val Gly Met Arg Cys Thr	
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys	Asp Arg Val Ala Val Ala	
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro	
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu	Arg Asp Phe Tyr Ser Pro	
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu	Ile Gly Glu Ala Leu Tyr	
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser	Leu Ile Ala Gly Ile Ile	
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg	Asn Arg Ser Asn Tyr Tyr	
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala	Thr Arg Ser Ser Pro Arg	
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser	Glu Phe Asn Ser Tyr Ser	
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
 gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50
 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
 aagtcacgcg tcccgctggc tcagaacccat ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcga atgtggtccc ccctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accaccaga gccatggctc cccgaggctg catcgtagct 50
 gtctttgccca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgtgcc cctggacatt catggtgaag ctgataaacc 300
 agaactgcga ctacagcccg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgtttacct gagatctggg atgctgagtg 450
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataatgaaa a 771

<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens.

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
 20 25 30
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
 35 40 45
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
 50 55 60
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
 65 70 75
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
 80 85 90
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
 95 100 105
 Cys Arg Ser Val Ser
 110

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139

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 gctcgcaactc agtcgcgga ggcttccccg cgccggccgc gtcccgccc 100
 ctccccgga ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgcctctcgc 200
 tctcttctcg gctgcgtccc taggtccggg ggcagccttc aaggctcgca 250
 cgccgtatcc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cagcatgtga ccttctacaa 350
 gacgtggtac cgcagctcga gggcgagggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcacg ttccaggacc ttacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900
 ataccgagg ccaaagtcag gcacccctg tcctatgtgg cccagcgga 950
 gccttctgag tctggggcgc atctgcttcc ggagcccagc acccccctgt 1000
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050
 gactctcaa actttgagggt catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250
 atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
 ccccggtggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550
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 gtccccagag cttggtgggc ccgaaacggg aagtacatat tggggcatgg 1750
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 gttgccccac cacttgagga tgggtgctgag ggaggtgggt ggggccttct 1850
 ggggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccaactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

	140		145		150
Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met	Glu		
	155		160		165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val		
	170		175		180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala		
	185		190		195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu		
	200		205		210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg		
	215		220		225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile		
	230		235		240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro		
	245		250		255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln		
	260		265		270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro		
	275		280		285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp		
	290		295		300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile			
	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgcc ctcttttctt gccaccgct gcttcttggc 150
 ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcggcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggccccct gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcgggtat cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaattcttc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggctcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

[illegible]

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys
440	445	450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cggggagctc ccgtggggcg tccgctggct gtgcaggcgg ccatggattc 100
 cttgctggaaa atgctgatct cagtcgcaat gctgggagca ggggctggcg 150
 tgggctacgc gtcctcggtt atcgtgaccc cggaagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttg cggaagggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400
 gaccttggtt tgggagcagg aatccgaggc agcctttctc cttcgtgggc 450

gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaaa tcatgtttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile
				335					340					345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala
				350					355					360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu
				365					370					375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly
				380					385					390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu
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Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctctctt tctctctaata ccatccgtca cctctcctgt catccgtttc 150
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 agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

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Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30

Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45

Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60

Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75

Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90

Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105

Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120

Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135

Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150

Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165

Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180

Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195

Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210

Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225

Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

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<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
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<400> 149
gcgtgggtcca cctctacagg gacg 24
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```
<210> 150
<211> 23
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

```
<400> 150
ggaactgacc cagtgctgac acc 23
```

```
<210> 151
<211> 45
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

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<400> 151
gcagatgccacagtatcaaggcaggacaaaactggtgaaggattc45
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<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens
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<400>	152					
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gcctcggcgg	ggaatgtcac	cggtggcggc	ggggccgcgg	ggcaggtgga	250	
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accgtccacc	gacccttggc	tgcgacttct	ccagcccagt	ccccggagac	400	

cacccctott tgggcgactg ctggaccctc ttcaccacc tttcaggcgc 450
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Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
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 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens
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<400> 160
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Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
          20          25          30

Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
          35          40          45

Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
          50          55          60

Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
          65          70          75

Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
          80          85          90

Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
          95          100          105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

```


Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
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Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

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tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccgga 550
acactaggca gcccccggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650
gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20		25		30
Val Lys Ala Met	Val Val Asp Lys Asp Phe	Pro Glu Asp Arg Arg			
	35	40		45	
Pro Arg Lys Val	Ser Pro Val Lys Val Thr	Ala Leu Gly Gly Gly			
	50	55		60	
Lys Leu Glu Ala	Thr Phe Thr Phe Met Arg	Glu Asp Arg Cys Ile			
	65	70		75	
Gln Lys Lys Ile	Leu Met Arg Lys Thr Glu	Glu Pro Gly Lys Tyr			
	80	85		90	
Ser Ala Tyr Gly	Gly Arg Lys Leu Met Tyr	Leu Gln Glu Leu Pro			
	95	100		105	
Arg Arg Asp His	Tyr Ile Phe Tyr Cys Lys	Asp Gln His His Gly			
	110	115		120	
Gly Leu Leu His	Met Gly Lys Leu Val Gly	Arg Asn Ser Asp Thr			
	125	130		135	
Asn Arg Glu Ala	Leu Glu Glu Phe Lys Lys	Leu Val Gln Arg Lys			
	140	145		150	
Gly Leu Ser Glu	Glu Asp Ile Phe Thr Pro	Leu Gln Thr Gly Ser			
	155	160		165	
Cys Val Pro Glu	His				
	170				

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

 <400> 165
 gtcctccgga aagtccttat c 21

 <210> 166
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 166
 gcctagtgtt cggaacgca gcttc 25

 <210> 167
 <211> 50
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

 <400> 167
 caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

 <210> 168
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 168
 ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

 <210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

 <400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcacgagg 50
cagaggtctc acagcagcca aggaacctgg ggccccctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccaactgagtc cttccccac ccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
ctcacgctgt gtcaactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tgggtgtttg ttctgtttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattcttttg gctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
20 25 30
His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
35 40 45
Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
50 55 60
Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
65 70 75
Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
80 85 90
Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
95 100 105
Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
110 115 120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
125 130 135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
140 145 150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
155 160 165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
170 175 180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
185 190 195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
200 205 210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
215 220 225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
230 235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
245 250

<210> 171
<211> 25
<212> DNA
<213> Artificial
<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 171
ggctgcgggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 176
 cccttgatga tcctgggc 18

<210> 177
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 177
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 178
 gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
 <211> 907
 <212> DNA
 <213> Homo sapiens

<400> 179
 gaggagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
 aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150
 agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
 atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
 caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcac 300
 aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
 aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

[illegible]

<210>	181
<211>	22
<212>	DNA
<213>	Artificial

```
<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.
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<400> 181
gtgttctgct ggagccgatg cc 22
```

```
<210> 182
<211> 18
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.
```

<400> 182
gacatggaca atgacagg 18

```
<210> 183
<211> 18
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.
```

```
<400> 183
ccttttcagga tqtaggag 18
```

```
<210> 184
<211> 18
<212> DNA
<213> Artificial
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<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 184
 gatgtctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 185
 gcatcctgat atgacttgct acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

 <400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

 cc 52

 <210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

 ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcc 100

cccaaatgct tctgtgtca ataacactca ctgcacctgc aaccatggat 150
atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
aacgccaggc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
ttcttgtttc atttcgcgac tgccctctca gtgtttcttg ggatcccctc 550
ccaaataaag tacttatatt ctc 573

<210> 189
<211> 74
<212> PRT
<213> Homo sapiens

<400> 189
Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15
Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30
Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45
Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60
Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 190
agggaccatt gcttcttcca ggcc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
    cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
    cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
    caagcagggtc atccccttgg tgaccttcaa agagaagcag agaggggcaga 50
    ggtgggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
    gactttggaa gtgaccacc atgggggtca gcatcttttt gctcctgtgt 150
    gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
    gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
    gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
    gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
    cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
    cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
    ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
    gcccctgccc aatgactgtg caaccgctgg caccgagtgc cactctcag 550
    gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
    tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
    cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700
    atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750
    caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

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ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatacattc 950
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val	Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp			
	215	220		225	
Gly Ile Pro Gly	Val Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp			
	230	235		240	
Ile Arg Met Ile	Met Arg Asn Asn				
	245				

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
ctcgccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
tcagtgaac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
tgccctgagg acccgcctg gactccccag cttcccacc ccatacctcc 600
ctccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
tttgtttggt cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700
agcaciaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
ttgggtcccc tccctctctt ctccctcct tccccgctcc ctgtgcagaa 800
gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggaggg 850
cttcagcct gtgttccct cacttgagg aaccagcact ctccatcctt 900
tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
gaccccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
 attccacacc tcttctcatc ctcagtgatg tgaagggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagaggggt tcggaggcag aagtgaggcc 1300
 tgggggtttg ggggaaagggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

cgcgctcccc gcgcgcctcc tcgggctcca cgcgtcttgc cccgcagagg 50
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggtcggcg ccgccgtgcg cgcgcgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagcgcgcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatcccga ggaaggcggt ccgcggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtgcctc ctggtcacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850
cagaagaagg agtacgtgtg cccagcccc cactcggagc ccccatcctg 900
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aagacaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
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Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser
	470	475 480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe	
	485	490 495
Ser Ser Glu Cys	Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg	
	500	505 510
Cys Glu Gly Thr	Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg	
	515	520 525
Ile Pro Ser His	Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn	
	530	535 540
Asp Asn Glu Val	Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys	
	545	550 555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys	
	560	565 570
Glu Val Arg Glu	Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu	
	575	580 585
Leu Met Leu Thr	Gly Asn Gln Leu Glu Thr Val His Gly Arg Val	
	590	595 600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn	
	605	610 615
Leu Ile Ser Cys	Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser	
	620	625 630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr	
	635	640 645
Pro Gly Ala Phe	Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu	
	650	655 660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly	
	665	670 675
Lys Trp Leu Arg	Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys	
	680	685 690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala	
	695	700 705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln	
	710	715 720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val	
	725	730 735
Val Arg Cys Ser	Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met	
	740	745 750

[illegible]

Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly	1040	1045	1050
1055	1060	1065	
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala	1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly	1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu	1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln	1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu	1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu	1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu	1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln	1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp	1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu	1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val	1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr	1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys	1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser	1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala	1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys	1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala	1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys	1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
atggagattc ctgccaaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
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cctgtgtcat cttgtcccg ttcctcccaa tattccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaat 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.'

<400> 205
ctcattggct gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
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<223> Synthetic construct.

<400> 208
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<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

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cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
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ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
tactgtcat ctgtaggga atttttgttt gtccctgtctt tgccctggatc 1550
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actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

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<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
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 cttcgcgata ttgcgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 tctaccteta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaa 200
 tttgcatgag ttcttggtta atttgcatga gagatatggg cctgtggtct 250
 ccttctggtt tggcagggcg ctcgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtga 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaagga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatggtg 1500
aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
ttaa 1554

<210> 212
<211> 462
<212> PRT
<213> Homo sapiens

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1 5 10 15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
20 25 30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
35 40 45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
50 55 60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
65 70 75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
80 85 90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
95 100 105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
110 115 120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
125 130 135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
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tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100
tcagggcttg tgccctctcg ctctctgacg ctctggcgcg atctggtggt 150
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgtctt ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggtcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
tgaggagtgc ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
tcccggaccc tgccgccttg ccactatgtc ccgccgtctc atgctgcttg 50
cctgggctct cccagcctc cttcgactcg gagcgggtca ggagacagaa 100
gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc aggtctact gcctgcggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

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tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
caattccaac acaatgccac agggcaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
ctcccgagac cagctcaga gctcagccac ctggagctgc tcccagccct 700
tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggtg 750
gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
cccatctggg tgacccgggg caggccacag aggccaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900
gttgggcctc aggcaggag ggggggtggag acgaggagat gccaagtggg 950
gccagggccca agtctcaagt ggagagaaa ggggtccaag tgctgggtccc 1000
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ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
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gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
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gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
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tcacctgtca gaccgggggtt ctcccggtac tggatggcgc cgcctctca 1700
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aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
1 5 10 15
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219
<211> 2065
<212> DNA
<213> Homo sapiens

<400> 219
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gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200
gcgccgccgc cgccgtcgct cctgcagcgc tgtcgacctc gccgctagca 250
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ggctgcccgct ctgggcacag aacgacacg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500
ctcttctcc ccgctgggga tatcggtccg ggcgccaac tccaaggtcg 550
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aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tggtactcgt gaagctgcc acaatggtgt cctgctctac ctagataaag 850
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ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg ttttttattg gtttctcatg 1050
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
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gaattttatt tgttttagtt taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgccaa 1350
agaactgtat actgtgttaa tatattgatt atatttgatt ttattccttt 1400
ggaattagtt tgtttgggtc ttgtaaaaaa ctgggatttt ttttttcagt 1450
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gaatgottca tagttgtatt ttaattgtat atgtgaaaga gtcataatttt 1600
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700
cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750
aatgattgat aataaccact ttattaataaa cctaagggtt tttttttttc 1800
cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
ttataacctat ttttcaaggc ttctgttgta tttgaagtat catctggttt 1900
tgccttaact ctttaaatg tatatatatta tctgttttagc taatattaaa 1950
ttcaaataat ccataatctaa atttagtgca atatcttgct tttgttatag 2000
gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
tatatgttaa aaaaa 2065

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
1 5 10 15
Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cggtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	1	5	10	15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	20	25	30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	50	55	60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	95	100	105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	110	115	120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	125	130	135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	140	145	150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	155	160	165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	170	175	180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	185	190	195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	200	205	210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	215	220	225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	230	235	240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	245	250	255	

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
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<212> PRT
<213> Homo sapiens

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 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
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 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
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 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
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 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
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 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
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 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
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 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
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 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr
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Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
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Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
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<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Ser	Gly	Lys	Ala	Thr	65	Glu	Gly	Pro	Phe	Ala	70	Met	Asp	Pro	Asp	Ser	75
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Ser	Arg	Gly	Thr	Arg	140	Pro	Gly	Ile	Pro	Phe	145	Leu	Phe	Leu	Glu	Ala	150
Ser	Asp	Arg	Asp	Glu	155	Pro	Gly	Thr	Ala	Asn	160	Ser	Asp	Leu	Arg	Phe	165
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Thr	Ala	Thr	Val	Glu	230	Val	Ser	Ile	Ile	Glu	235	Ser	Thr	Trp	Val	Ser	240
Leu	Glu	Pro	Ile	His	245	Leu	Ala	Glu	Asn	Leu	250	Lys	Val	Leu	Tyr	Pro	255
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Phe	Gln	Val	Asp	Pro 395	Thr	Ser	Gly	Ser	Val 400	Thr	Leu	Gly	Val	Leu 405
Pro	Leu	Arg	Ala	Gly 410	Gln	Asn	Ile	Leu	Leu 415	Leu	Val	Leu	Ala	Met 420
Asp	Leu	Ala	Gly	Ala 425	Glu	Gly	Gly	Phe	Ser 430	Ser	Thr	Cys	Glu	Val 435
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Pro	Gly	Pro	Gly	Pro 545	Gly	Ala	Thr	Ala	Thr 550	Val	Thr	Val	Leu	Val 555
Glu	Arg	Val	Met	Pro 560	Pro	Pro	Lys	Leu	Asp 565	Gln	Glu	Ser	Tyr	Glu 570
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Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
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Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
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Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
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Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
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Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
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Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
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Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
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Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
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Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
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<212> DNA
<213> Homo sapiens
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<400>	233				
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cagaaatgga	gacgagatca	gcaaattgag	tcaactagtg	aattcaaaca	150
acttgaagct	caattttctg	aaatctccct	cctccttcaa	tgggcctgtg	200
gatgtcctgg	tcccatctgt	cagtctgcag	gcattttaat	ccttcctgag	250
atcccagggc	ttagagtagc	cagtgacaat	tgaggacctg	caggcccttt	300
tagacaatga	agatgatgaa	atgcaacaca	atgaagggca	agaacggagc	350
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cgagatggac	aacattgccg	cagactttcc	tgacctggcg	aggaggggtga	450
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atggatatatt	tcttgttgcc	tgtggccaat	cctgatggat	atgtgtatac	700
tcaaactcaa	aaccgattat	ggaggaagac	gcgggtccga	aatcctggaa	750
gctcctgcat	tggtgctgac	ccaaatagaa	actggaacgc	tagttttgca	800
ggaaagggag	ccagcgacaa	cccttgctcc	gaagtgtacc	atggacccca	850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
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 atgtatccat atgggtactc agtcaaaaag gcccagatg ccgaggaact 1000
 cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
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 agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
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 catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
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<210> 234
<211> 421
<212> PRT
<213> Homo sapiens
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<400>	234															
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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn		
				20					25					30		
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn		
				35					40					45		
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe		
				50					55					60		
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala		
				65					70					75		
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr		
				80					85					90		
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met		
				95					100					105		
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr		
				110					115					120		
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn		
				125					130					135		
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly		
				140					145					150		
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr		
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<400> 235

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 cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
 aacaccgact ttgccttccg cctataccgc aggctgggtt tggagacccc 250
 gagtcagaac atctttcttct cccctgtgag tgtctccact tccctggcca 300
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 ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450
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 tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220 225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235 240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250 255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265 270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280 285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295 300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310 315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325 330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340 345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355 360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370 375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385 390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400 405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415

<210> 237
 <211> 23
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.
 <400> 237
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 <210> 238

<211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 238
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 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 239
 tgactcgggg tctccaaaac cagc 24

 <210> 240
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 240
 ggtataggcg gaaggcaaag tcgg 24

 <210> 241
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

 <400> 241
 ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

 <210> 242
 <211> 2436
 <212> DNA
 <213> Homo sapiens

 <400> 242
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ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
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tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
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tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
<211> 596
<212> PRT
<213> Homo sapiens

<400> 243
Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
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Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
20 25 30
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
35 40 45
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
50 55 60
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
65 70 75

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165
 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240
 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270
 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala		
	380	385	390		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala		
	395	400	405		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala		
	410	415	420		
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala		
	425	430	435		
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val		
	440	445	450		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala		
	455	460	465		
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470	475	480		
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485	490	495		
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500	505	510		
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515	520	525		
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530	535	540		
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545	550	555		
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560	565	570		
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575	580	585		
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590	595			

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.
 <400> 244

gaagcaccag cctttatctc ttcacc 26
 <210> 245
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.
 <400> 245
 gtcagagttg gtggctgtgc tagc 24
 <210> 246
 <211> 48
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.
 <400> 246
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48
 <210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens
 <400> 247
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 tccctccttc tgctactggg gccctgtct ggatgggcgg ccagcgatga 150
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
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gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
tacacca 957

<210> 248
<211> 247
<212> PRT
<213> Homo sapiens

<400> 248
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
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Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
 185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
 200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
 215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 230 235 240

Ser Val Ala Asn Ile Met Pro
 245

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 249
 caatatgcat cttgcacgctc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 251
 tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252

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ggggcggaac gcggggcgga gctgcgcgcc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgtccc tgctctccga atgctgcgca 250
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 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

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Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile			
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Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
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Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
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Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
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Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
				800										

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
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<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc	aatcctatca	gtgaagaaac	tacaactttc	cctacaggag	450
gcttcacacc	ggaaatagga	aagaaaaaac	acacggaaag	taccccatte	500
tggtcgatca	aaccaaaca	tgtttccatt	gttttgcattg	cagaggaacc	550
ttatattgaa	aatgaagagc	cagagccaga	gccggagcca	gctgcaaaac	600
aaactgaggc	accaagaatg	ttgccagttg	ttactgaatc	atctacaagt	650
ccatatgtta	cctcatataa	gtcacctgtc	accactttag	ataagagcac	700
tggcattgag	atctctacag	aatcagaaga	tgttcctcag	ctctcaggtg	750
aaactgcgat	agaaaaaccc	gaagagtttg	gaaagcacc	agagagttgg	800
aataatgatg	acattttgaa	aaaaatttta	gatattaatt	cacaagtgca	850
acaggcaactt	cttagtgaca	ccagcaaccc	agcatataga	gaagatatgtg	900
aagcctctaa	agatcaccta	aaacgaagcc	ttgctctagc	agcagcagca	950
gaacataaat	taaaaaacaat	gtataagtcc	cagttattgc	cagtaggacg	1000
aacaagtaat	aaaattgatg	acatcgaaac	tgttattaac	atgctgtgta	1050
attctagatc	taaactctat	gaatatattag	atattaaatg	tgttccacca	1100
gagatgagag	aaaaagctgc	tacagtattc	aatacattaa	aaaatatgtg	1150
tagatcaagg	agagtcacag	ccttattaaa	agtttattaa	acaataatat	1200
aaaaatttta	aacctacttg	atattccata	acaaagctga	tttaagcaaa	1250
ctgcattttt	tcacaggaga	aataatcata	ttcgtaattt	caaaagttgt	1300
ataaaaaatat	tttctattgt	agttcaaagt	tgccaacatc	tttatgtgtc	1350
atgtgttatg	aacaattttc	atatgcacta	aaaaccta	ttaaaaataa	1400
attttggttc	aggaaaaaa	1419			

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<210> 265
<211> 350
<212> PRT
<213> Homo sapiens
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<400> 265
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Ser  Val  Pro  Ala  Tyr  Pro  Ser  Ile  Thr  Val  Thr  Pro  Asp  Glu  Glu
          20          25          30
Gln  Asn  Leu  Asn  His  Tyr  Ile  Gln  Val  Leu  Glu  Asn  Leu  Val  Arg
          35          40          45
Ser  Val  Pro  Ser  Gly  Glu  Pro  Gly  Arg  Glu  Lys  Lys  Ser  Asn  Ser

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50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Lys	Gly	Ser	Lys	Phe	Lys				
				65					70						75				
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85						90				
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100						105				
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115						120				
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130						135				
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145						150				
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160						165				
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175						180				
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190						195				
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205						210				
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220						225				
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235						240				
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250						255				
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265						270				
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280						285				
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295						300				
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310						315				
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325						330				
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
				335					340						345				


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ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg 1350
agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500
tcccatattc atatgtccag tgcctgggg atgagacaga gaagaccctg 1550
cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600
ccgacaggtg gcccagctt cctctcggga gcctgcgcac agagagtcac 1650
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ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
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aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcatataca cagacacaaa aattctaaat aaaattttta 2250
caaattaaac taaacaatat atttaaagat gatataatac tactcagtgt 2300
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gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
  1             5             10             15

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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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20					25					30				
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaataatgc 300
atattataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcgtt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt ttacaacat ataagaaccc 750
tgccagatgg actgcttctt ttggagtaac aataaacct tcgaaaatga 800
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aatgacgta catagagttt gtctccctga tgcctcctat gagtttcaac 950
caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggatgactct 1150
ggaggaccac tgggttagttc agatgctaga gatattctgt acccttgctgg 1200
aatagtgagc tggggagatg aatgtgcaaa acccaacaag cctgggtgttt 1250
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cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
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aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccaactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
 ttccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggtgtgcc cctgcgaacta 300
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagaggggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gaccgcgcgc gcatgggaga agtgcgcatc gcggccgaag agggccgcgc 450
agtgggtccac tgggtgtgcc ccttctcccc ggtcctccac tactggctgc 500
tgctttggga cggcagcgag gctgcgaga aggggcccc gctgaacgct 550
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cgtttgcgta gtggccgcta acgagggcgg ggcaagccgc gtgccccagg 650
ctggaggaga gggcctcgag ggggcccaga tcctgcctt cgggccttgc 700
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gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900
ccccacctgg ggcgtcagc ctggcccccg ggaaagagga aaacccgctg 950
cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000
gccacggcgg agtcatggtt ctgaggactg agcgcttggt taggtccggt 1050
acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
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ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

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<211> 2397
<212> DNA
<213> Homo sapiens

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aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
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Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
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Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
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Glu Met Glu Glu	Leu				
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<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	185	190	195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	200	205	210	
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	215	220	225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	230	235	240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	245	250	255	

Gly Ser Asp Lys	Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	
260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	
275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	
290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	
305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	
320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	
335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	
350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	
365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	
380	385	390
Asp Gln Trp His	Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	
395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	
410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys Ala Glu Leu	
425	430	

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 <212> DNA
 <213> Homo sapiens

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 <211> 761
 <212> PRT
 <213> Homo sapiens
 <400> 277

[illegible]

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Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val
				320					325					330
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp
				335					340					345
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu
				350					355					360
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg
				365					370					375
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr
				380					385					390
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr
				395					400					405
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val
				410					415					420
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr
				425					430					435
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly
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Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp
				455					460					465
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala
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Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu
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Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg
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Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser
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Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala
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Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala
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Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
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<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 279
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<210> 280
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<220>
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<223> Synthetic construct.

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<212> DNA
<213> Homo sapiens

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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
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 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

					260					265					270
Leu	Met	Glu	Lys		Pro 275	Ile	Lys	Pro	Val	Pro 280	Gln	Asp	Leu	Glu	Asn 285
Phe	Ile	Ala	Lys		Phe 290	Gly	Asp	Ser	Gly	Phe 295	Val	Leu	Val	Thr	Leu 300
Gly	Ser	Met	Val		Asn 305	Thr	Cys	Gln	Asn	Pro 310	Glu	Ile	Phe	Lys	Glu 315
Met	Asn	Asn	Ala		Phe 320	Ala	His	Leu	Pro	Gln 325	Gly	Val	Ile	Trp	Lys 330
Cys	Gln	Cys	Ser		His 335	Trp	Pro	Lys	Asp	Val 340	His	Leu	Ala	Ala	Asn 345
Val	Lys	Ile	Val		Asp 350	Trp	Leu	Pro	Gln	Ser 355	Asp	Leu	Leu	Ala	His 360
Pro	Ser	Ile	Arg		Leu 365	Phe	Val	Thr	His	Gly 370	Gly	Gln	Asn	Ser	Ile 375
Met	Glu	Ala	Ile		Gln 380	His	Gly	Val	Pro	Met 385	Val	Gly	Ile	Pro	Leu 390
Phe	Gly	Asp	Gln		Pro 395	Glu	Asn	Met	Val	Arg 400	Val	Glu	Ala	Lys	Lys 405
Phe	Gly	Val	Ser		Ile 410	Gln	Leu	Lys	Lys	Leu 415	Lys	Ala	Glu	Thr	Leu 420
Ala	Leu	Lys	Met		Lys 425	Gln	Ile	Met	Glu	Asp 430	Lys	Arg	Tyr	Lys	Ser 435
Ala	Ala	Val	Ala		Ala 440	Ser	Val	Ile	Leu	Arg 445	Ser	His	Pro	Leu	Ser 450
Pro	Thr	Gln	Arg		Leu 455	Val	Gly	Trp	Ile	Asp 460	His	Val	Leu	Gln	Thr 465
Gly	Gly	Ala	Thr		His 470	Leu	Lys	Pro	Tyr	Val 475	Phe	Gln	Gln	Pro	Trp 480
His	Glu	Gln	Tyr		Leu 485	Phe	Asp	Val	Phe	Val 490	Phe	Leu	Leu	Gly	Leu 495
Thr	Leu	Gly	Thr		Leu 500	Trp	Leu	Cys	Gly	Lys 505	Leu	Leu	Gly	Met	Ala 510
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275

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
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<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

[illegible]

					170						175					180
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser		
				185					190					195		
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu							
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<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 288
 aggcagccac cagctctgtg ctac 24

 <210> 289
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 289
 cagagagggg agatgaggaa gccagag 27

 <210> 290
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

 <400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

 <210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

 <400> 291
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 aaaaaaaaaa aaaaaaaaaa 1570

Ala Asp Leu Val	Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val	Tyr
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Lys Gln Val Ile	Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val	Gln
290		295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe	His
305		310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro	Tyr
320		325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly	Glu Pro Ile Thr Ile	Pro
335		340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His	Thr
350		355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu	Phe Asp Lys His Lys	Thr
365		370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val	Leu Glu Val Asn	
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<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
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 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
170 175 180

Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
185 190 195

Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
200 205 210

Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
215 220 225

Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
230 235 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
245 250 255

Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
260 265 270

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
275 280 285

Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
290 295 300

Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
305 310 315

Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
320 325 330

Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
335 340 345

Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
350 355 360

Glu Pro Gly Arg Trp Arg Leu Gln
365

<210> 298
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 298
cttcctctgt ggggtggacca tgtg 24

<210> 299
<211> 21
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
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<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
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 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
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 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
 65 70 75
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
 80 85 90
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
 95 100 105
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
 110 115 120
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
 125 130 135
 Cys Gly Val Leu Leu Ser Phe Leu

140

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

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tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
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<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
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 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
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Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90
Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105
Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120
Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135
Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150
Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165
Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180
Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195
Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210
Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225
Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240
Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255
Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
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ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
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actataaacg gttttttaat ga 2272

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
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Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

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Asp Asn Ser Gly	Leu 155	Lys Arg Lys Thr	Pro 160	Ala Leu Lys Met	Ser 165
Val Ser Lys Arg	Ala 170	Arg Lys Ala Ser	Ser 175	Asp Leu Asp Gln	Ala 180
Ser Val Ser Pro	Ser 185	Glu Glu Glu Asn	Ser 190	Glu Ser Ser Ser	Glu 195
Ser Glu Lys Thr	Ser 200	Asp Gln Asp Phe	Thr 205	Pro Glu Lys Lys	Ala 210
Ala Val Arg Ala	Pro 215	Arg Arg Gly Pro	Leu 220	Gly Gly Arg Lys	Lys 225
Lys Lys Ala Pro	Ser 230	Ala Ser Asp Ser	Asp 235	Ser Lys Ala Asp	Ser 240
Asp Gly Ala Lys	Pro 245	Glu Pro Val Ala	Met 250	Ala Arg Ser Ala	Ser 255
Ser Ser Ser Ser	Ser 260	Ser Ser Ser Ser	Asp 265	Ser Asp Val Ser	Val 270
Lys Lys Pro Pro	Arg 275	Gly Arg Lys Pro	Ala 280	Glu Lys Pro Leu	Pro 285
Lys Pro Arg Gly	Arg 290	Lys Pro Lys Pro	Glu 295	Arg Pro Pro Ser	Ser 300
Ser Ser Ser Asp	Ser 305	Asp Ser Asp Glu	Val 310	Asp Arg Ile Ser	Glu 315
Trp Lys Arg Arg	Asp 320	Glu Ala Arg Arg	Arg 325	Glu Leu Glu Ala	Arg 330
Arg Arg Arg Glu	Gln 335	Glu Glu Glu Leu	Arg 340	Arg Leu Arg Glu	Gln 345
Glu Lys Glu Glu	Lys 350	Glu Arg Arg Arg	Glu 355	Arg Ala Asp Arg	Gly 360
Glu Ala Glu Arg	Gly 365	Ser Gly Gly Ser	Ser 370	Gly Asp Glu Leu	Arg 375
Glu Asp Asp Glu	Pro 380	Val Lys Lys Arg	Gly 385	Arg Lys Gly Arg	Gly 390
Arg Gly Pro Pro	Ser 395	Ser Ser Asp Ser	Glu 400	Pro Glu Ala Glu	Leu 405
Glu Arg Glu Ala	Lys 410	Lys Ser Ala Lys	Lys 415	Pro Gln Ser Ser	Ser 420
Thr Glu Pro Ala	Arg 425	Lys Pro Gly Gln	Lys 430	Glu Lys Arg Val	Arg 435

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Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
440                               445                               450
Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
455                               460                               465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
470                               475                               480
Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
485                               490                               495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
500                               505                               510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
515                               520                               525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
530                               535                               540
Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
545                               550                               555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
560                               565                               570
Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
575                               580                               585
Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
590                               595                               600
Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
605                               610                               615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
620                               625                               630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
635                               640                               645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
650                               655                               660
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<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

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<400> 309
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cagcctcaat aattatatta aattaacacc atttgaaaga gaacattgtt 100

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ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
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 tacaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300
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 tcactcctgg agaatggtat aggaatttgg agaggtgcat tatttctttc 3000

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<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 20 25 30
 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80									85					90	
Phe	Leu	Leu	Ser	Leu 95	Val	Asp	Leu	Asn	Lys 100	Asn	Phe	Lys	Lys	Ile 105	
Tyr	Trp	Pro	Ala	Ala 110	Lys	Glu	Arg	Val	Glu 115	Leu	Cys	Lys	Leu	Ala 120	
Gly	Lys	Asp	Ala	Asn 125	Thr	Glu	Cys	Ala	Asn 130	Phe	Ile	Arg	Val	Leu 135	
Gln	Pro	Tyr	Asn	Lys 140	Thr	His	Ile	Tyr	Val 145	Cys	Gly	Thr	Gly	Ala 150	
Phe	His	Pro	Ile	Cys 155	Gly	Tyr	Ile	Asp	Leu 160	Gly	Val	Tyr	Lys	Glu 165	
Asp	Ile	Ile	Phe	Lys 170	Leu	Asp	Thr	His	Asn 175	Leu	Glu	Ser	Gly	Arg 180	
Leu	Lys	Cys	Pro	Phe 185	Asp	Pro	Gln	Gln	Pro 190	Phe	Ala	Ser	Val	Met 195	
Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210	
Lys	Asp	Thr	Ala	Phe 215	Thr	Arg	Ser	Leu	Gly 220	Pro	Thr	His	Asp	His 225	
His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240	
Ala	Lys	Phe	Ile	Gly 245	Thr	Phe	Phe	Ile	Pro 250	Asp	Thr	Tyr	Asn	Pro 255	
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Arg 265	Glu	Ser	Ser	Gln	Glu 270	
Gly	Ser	Thr	Ser	Asp 275	Lys	Thr	Ile	Leu	Ser 280	Arg	Val	Gly	Arg	Val 285	
Cys	Lys	Asn	Asp	Val 290	Gly	Gly	Gln	Arg	Ser 295	Leu	Ile	Asn	Lys	Trp 300	
Thr	Thr	Phe	Leu	Lys 305	Ala	Arg	Leu	Ile	Cys 310	Ser	Ile	Pro	Gly	Ser 315	
Asp	Gly	Ala	Asp	Thr 320	Tyr	Phe	Asp	Glu	Leu 325	Gln	Asp	Ile	Tyr	Leu 330	
Leu	Pro	Thr	Arg	Asp 335	Glu	Arg	Asn	Pro	Val 340	Val	Tyr	Gly	Val	Phe 345	
Thr	Thr	Thr	Ser	Ser 350	Ile	Phe	Lys	Gly	Ser 355	Ala	Val	Cys	Val	Tyr 360	
Ser	Met	Ala	Asp	Ile 365	Arg	Ala	Val	Phe	Asn 370	Gly	Pro	Tyr	Ala	His 375	

300

[illegible]

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

				665					670					675
Ile	Val	Lys	Leu	Thr 680	Leu	Asn	Val	Ile	Glu 685	Asn	Glu	Gln	Met	Glu 690
Asn	Thr	Gln	Arg	Ala 695	Glu	His	Glu	Glu	Gly 700	Gln	Val	Lys	Asp	Leu 705
Leu	Ala	Glu	Ser	Arg 710	Leu	Arg	Tyr	Lys	Asp 715	Tyr	Ile	Gln	Ile	Leu 720
Ser	Ser	Pro	Asn	Phe 725	Ser	Leu	Asp	Gln	Tyr 730	Cys	Glu	Gln	Met	Trp 735
His	Arg	Glu	Lys	Arg 740	Arg	Gln	Arg	Asn	Lys 745	Gly	Gly	Pro	Lys	Trp 750
Lys	His	Met	Gln	Glu 755	Met	Lys	Lys	Lys	Arg 760	Asn	Arg	Arg	His	His 765
Arg	Asp	Leu	Asp	Glu 770	Leu	Pro	Arg	Ala	Val 775	Ala	Thr			

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<210> 311
<211> 25
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.
```

```
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caacgcagcc gtgataaaca agtgg 25
```

```
<210> 312
<211> 24
<212> DNA
<213> Artificial
```

```
<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
```

```
<400> 312
gcttggacat gtaccaggcc gtqq 24
```

```
<210> 313
<211> 45
<212> DNA
<213> Artificial
```

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<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
```

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

<400> 314
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ctcagcagtt tcagccagca gggactgac aggtgtgtgt cctggagtgg 200
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300
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cagaggggag ggaaaggat ttttaaggtaa cagtgtggca caatagttaa 450
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accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttcccg 1250

304

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<210> 315
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 315
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr
 1 5 10 15

Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala			

305 310 315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
335 340 345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
350 355 360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr
365 370

<210> 316
<211> 4407
<212> DNA
<213> Homo sapiens

<400> 316
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agacacaggc agggagagac aaagatccag gaaaggaggg ctgaggagga 200
gagtttgagg aagccagacc cctgggcacc tctcccaagc ccaaggacta 250
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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
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20 25 30
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro Leu	140	145	150
155	160			165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile	170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn	185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala	200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val	215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg	230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys His	245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	425	430	435

1

Val	Thr	Phe	Pro	Gly 440	Lys	Asp	Tyr	Asp	Ala 445	Asp	Arg	Gln	Cys	Gln 450
Leu	Thr	Phe	Gly	Pro 455	Asp	Ser	Arg	His	Cys 460	Pro	Gln	Leu	Pro	Pro 465
Pro	Cys	Ala	Ala	Leu 470	Trp	Cys	Ser	Gly	His 475	Leu	Asn	Gly	His	Ala 480
Met	Cys	Gln	Thr	Lys 485	His	Ser	Pro	Trp	Ala 490	Asp	Gly	Thr	Pro	Cys 495
Gly	Pro	Ala	Gln	Ala 500	Cys	Met	Gly	Gly	Arg 505	Cys	Leu	His	Met	Asp 510
Gln	Leu	Gln	Asp	Phe 515	Asn	Ile	Pro	Gln	Ala 520	Gly	Gly	Trp	Gly	Pro 525
Trp	Gly	Pro	Trp	Gly 530	Asp	Cys	Ser	Arg	Thr 535	Cys	Gly	Gly	Gly	Val 540
Gln	Phe	Ser	Ser	Arg 545	Asp	Cys	Thr	Arg	Pro 550	Val	Pro	Arg	Asn	Gly 555
Gly	Lys	Tyr	Cys	Glu 560	Gly	Arg	Arg	Thr	Arg 565	Phe	Arg	Ser	Cys	Asn 570
Thr	Glu	Asp	Cys	Pro 575	Thr	Gly	Ser	Ala	Leu 580	Thr	Phe	Arg	Glu	Glu 585
Gln	Cys	Ala	Ala	Tyr 590	Asn	His	Arg	Thr	Asp 595	Leu	Phe	Lys	Ser	Phe 600
Pro	Gly	Pro	Met	Asp 605	Trp	Val	Pro	Arg	Tyr 610	Thr	Gly	Val	Ala	Pro 615
Gln	Asp	Gln	Cys	Lys 620	Leu	Thr	Cys	Gln	Ala 625	Arg	Ala	Leu	Gly	Tyr 630
Tyr	Tyr	Val	Leu	Glu 635	Pro	Arg	Val	Val	Asp 640	Gly	Thr	Pro	Cys	Ser 645
Pro	Asp	Ser	Ser	Ser 650	Val	Cys	Val	Gln	Gly 655	Arg	Cys	Ile	His	Ala 660
Gly	Cys	Asp	Arg	Ile 665	Ile	Gly	Ser	Lys	Lys 670	Lys	Phe	Asp	Lys	Cys 675
Met	Val	Cys	Gly	Gly 680	Asp	Gly	Ser	Gly	Cys 685	Ser	Lys	Gln	Ser	Gly 690
Ser	Phe	Arg	Lys	Phe 695	Arg	Tyr	Gly	Tyr	Asn 700	Asn	Val	Val	Thr	Ile 705
Pro	Ala	Gly	Ala	Thr 710	His	Ile	Leu	Val	Arg 715	Gln	Gln	Gly	Asn	Pro 720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttggttcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttcact ttcttgccaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750
gacccgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaa tggaaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggaggggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcagctctat tcaatgaatt tctgcctatg aggcactctg 1100
ccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 323
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 cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtctacatg aaagggctct ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagt ccagatctac cgatccctgc 300
 tggcgtgccc ccaagacctc caggctgccc gcgcctcat ggtcatctcc 350
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cagcgcgtgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450
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 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
atatttatgt gggtgatttg ataacaagtt taatataaag tgacttgga 1100
gtttggtcag tgggggttggg ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
1 5 10 15
Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
20 25 30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
35 40 45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
50 55 60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
80 85 90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
95 100 105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
110 115 120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
125 130 135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
140 145 150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
155 160 165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
170 175 180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
185 190 195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
200 205 210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 325
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ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
cacatgccaa gtggtggcgt tctctctgtc catcctgggg ctggccggct 150
gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
aaccccgctca cctcogtggt ccagtacgaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350
gtcctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400
ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600
ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
gggggtgtga tgatgtgcat cgcctgccgg ggctggcac cagaagaaac 700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
tccttccaag cagactatg tgtaatgtc taagacctct cagcacgggc 900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
atctcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
atcttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
gagaatgtgg ttttaatctc tctctcacat ttgatgatt tagacagaact 1200
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tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
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cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
atTTTTTTta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
aaagtcatgc ttaagtacaa attocatgaa aagctcacac ctgtaatcct 1800
agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
aggttaaaac taattcttta a 2121

<210> 326
<211> 261
<212> PRT
<213> Homo sapiens

<400> 326
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
1 5 10 15
Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
20 25 30
Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
35 40 45
Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
50 55 60
Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
65 70 75
Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tggtggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400
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 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgctg 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaaact ttgatttaact gttcttaact gcctaattctt aattacagga 900
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacct aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcatataga gacatgctta 1150
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 actcaactat tgctttttcag ggaaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
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 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
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 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850
ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
ttttctaatt 2010

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<210> 328
<211> 225
<212> PRT
<213> Homo sapiens
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<400>	328														
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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	
				20					25					30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	
				35					40					45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	
				50					55					60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	
				80					85					90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	
				95					100					105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	
				110					115					120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	
				125					130					135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	
				140					145					150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	
				155					160					165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	
				170					175					180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	
				185					190					195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	
				200					205					210	

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
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Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
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<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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Ala Leu Met Cys	Val Ala Val Ala Leu	Ser Leu Ile Ala Leu	Leu
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val	Gln Cys Thr Gly Ser	Asn
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly	Thr Ser Gly Val Leu	Phe
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile	Pro Val Ser Trp Thr	Ala
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn	Pro Ala Ile His Ile	Gly
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu	Phe Leu Gly Trp Ala	Ser
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly	Leu Leu Cys Gly Phe	Cys
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr	Arg Tyr Pro Val Pro	Gly
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg	Arg Asn Thr Thr Met	Leu
	155	160	165
Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctcaaaaaa agtggactgc agcattttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
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<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
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 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

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 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
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 Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

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<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
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 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
50 55 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
65 70 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
80 85 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
95 100 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
170 175 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
185 190 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
200 205 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
215 220 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
230 235 240

Phe Ala Met Tyr Arg Pro
245

<210> 339
<211> 849
<212> DNA
<213> Homo sapiens

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<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
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20 25 30
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

140

145

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
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<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
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<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 343
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<210> 344
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 <212> DNA
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<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 344
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<210> 345
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 <212> DNA
 <213> Artificial

332

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 345

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<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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[illegible]

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
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Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

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Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
                110                115                120

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Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
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Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His
275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile
290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile
305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg
320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro
335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg
350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr
365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly
380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly
395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln
410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg
425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu
440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala
455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu
470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu
485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His
500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp
515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg
530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
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Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
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Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
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<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
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<220>
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338

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tcaaataaag cctttgcaag ataa 2524

<210> 352
<211> 243
<212> PRT
<213> Homo sapiens

<400> 352
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
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 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
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 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
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 Leu Pro Lys

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 <211> 480
 <212> DNA
 <213> Homo sapiens

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<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
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 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
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agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggg 450
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aacctgacct	tggaagatgc	tgctgagtgt	ctcaagcagc	actgacagca	1900
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cgaccccgga	cagagctgag	ctggccaggg	ccaggagggc	gggagggagg	2050
gaatgggggt	gggctgtgcg	cagcatcagc	gcctgggcag	gtccgcagag	2100
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<210> 356
<211> 157
<212> PRT
<213> Homo sapiens
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Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
  35          40          45
Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
  50          55          60
Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
  65          70          75
Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
  80          85          90
Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
  95          100          105
Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
  110          115          120
Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
  125          130          135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

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 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
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 cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358
 <211> 273
 <212> PRT
 <213> Homo sapiens

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 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
 35 40 45
 Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
 50 55 60
 Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
 65 70 75
 His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
 80 85 90
 Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
 95 100 105
 Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
 110 115 120
 Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
 125 130 135
 Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
 140 145 150
 Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
 155 160 165
 Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
 170 175 180
 Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
 185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgcc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

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<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
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cgggctgccg cccccggggg cttggcctca agctgcggac gacgcgggggt 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggcc 150
tcgggctggg gctggggctg gcgctcggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtcccccgcg gccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctgtgtca gaaggttttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

Trp	Ser	Pro	Gln	Thr 95	Pro	Ala	Pro	Pro	Cys 100	Ser	Arg	Cys	Phe	Ala 105
Arg	Ala	Ile	Glu	Ser 110	Ser	Arg	Asp	Leu	Leu 115	His	Arg	Ile	Lys	Asp 120
Glu	Val	Gly	Ala	Pro 125	Gly	Ile	Val	Val	Gly 130	Val	Ser	Val	Asp	Gly 135
Lys	Glu	Val	Trp	Ser 140	Glu	Gly	Leu	Gly	Tyr 145	Ala	Asp	Val	Glu	Asn 150
Arg	Val	Pro	Cys	Lys 155	Pro	Glu	Thr	Val	Met 160	Arg	Ile	Ala	Ser	Ile 165
Ser	Lys	Ser	Leu	Thr 170	Met	Val	Ala	Leu	Ala 175	Lys	Leu	Trp	Glu	Ala 180
Gly	Lys	Leu	Asp	Leu 185	Asp	Ile	Pro	Val	Gln 190	His	Tyr	Val	Pro	Glu 195
Phe	Pro	Glu	Lys	Glu 200	Tyr	Glu	Gly	Glu	Lys 205	Val	Ser	Val	Thr	Thr 210
Arg	Leu	Leu	Ile	Ser 215	His	Leu	Ser	Gly	Ile 220	Arg	His	Tyr	Glu	Lys 225
Asp	Ile	Lys	Lys	Val 230	Lys	Glu	Glu	Lys	Ala 235	Tyr	Lys	Ala	Leu	Lys 240
Met	Met	Lys	Glu	Asn 245	Val	Ala	Phe	Glu	Gln 250	Glu	Lys	Glu	Gly	Lys 255
Ser	Asn	Glu	Lys	Asn 260	Asp	Phe	Thr	Lys	Phe 265	Lys	Thr	Glu	Gln	Glu 270
Asn	Glu	Ala	Lys	Cys 275	Arg	Asn	Ser	Lys	Pro 280	Gly	Lys	Lys	Lys	Asn 285
Asp	Phe	Glu	Gln	Gly 290	Glu	Leu	Tyr	Leu	Arg 295	Glu	Lys	Phe	Glu	Asn 300
Ser	Ile	Glu	Ser	Leu 305	Arg	Leu	Phe	Lys	Asn 310	Asp	Pro	Leu	Phe	Phe 315
Lys	Pro	Gly	Ser	Gln 320	Phe	Leu	Tyr	Ser	Thr 325	Phe	Gly	Tyr	Thr	Leu 330
Leu	Ala	Ala	Ile	Val 335	Glu	Arg	Ala	Ser	Gly 340	Cys	Lys	Tyr	Leu	Asp 345
Tyr	Met	Gln	Lys	Ile 350	Phe	His	Asp	Leu	Asp 355	Met	Leu	Thr	Thr	Val 360
Gln	Glu	Glu	Asn	Glu 365	Pro	Val	Ile	Tyr	Asn 370	Arg	Ala	Arg		

<210> 367

<211> 30
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-30
 <223> Synthetic construct.

 <400> 367
 tggaaaagaa gtctgggtcag aaggttttagg 30

 <210> 368
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 368
 catttggtt cattctcctg ctctg 25

 <210> 369
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 369
 aaaacctcag aacaactcat tttgcacc 28

 <210> 370
 <211> 41
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

 <400> 370
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

 <210> 371
 <211> 1150
 <212> DNA
 <213> Homo sapiens

 <400> 371
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
50 55 60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
65 70 75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
80 85 90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
95 100 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
110 115 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
125 130 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
140 145 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
155 160 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
170 175 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
185 190 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
200 205 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
215 220 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
230 235 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
245 250 255

Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
260 265

<210> 373
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 373
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gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tgggaagggcc tgcagcaatc cctccttctc tcggttttcaa 250
ctggacttct atcagggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttaact cactatgctg ctttaacaaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttgggtgggct gtccacagcc 550
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gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
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tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
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ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tgggtgatggc tctgctggca gtgggtgggac 1400
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gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaaata gatcaaaaaa 1700

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<210> 374
<211> 450
<212> PRT
<213> Homo sapiens
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<400>	374													
Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggatgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
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gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatattggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
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cccagggccc ccaaggtgtg ctcatgctac aagaagaggc aagagacagg 850
ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376
<211> 188
<212> PRT
<213> Homo sapiens

<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15
Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30
Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45
Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

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 ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
 gccctgggat gcaccggcca gagggccatgc tgctgctgct cacgcttgcc 150
 ctcttggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggtctgc 250
 ggggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttggg 300
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
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 gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
 ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650
 ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
 actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
 gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
agctctgtgg ctgaactggg tgctcatcac ggggaactgct gggctatgga 100
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
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tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcttggg 400
tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc 450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
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cgaggatgcc ctaagggtg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatatctgct ggttgcttag 700
gtttgtccct tgcgtataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatacag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
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gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
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atcaattttc caagctcaac ctggcccttt ttccaagggtt ggtcagcctt 1200
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250
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tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaatctgcag 1350
cgctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
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ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
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aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
gggaccctgc acctataaca aatcgggctc caggagagtgt gaggtatgaa 2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
	215	220 225
Pro Arg Leu Val	Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys
	230	235 240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
	245	250 255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
	260	265 270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
	275	280 285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
	290	295 300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
	305	310 315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
	320	325 330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
	335	340 345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
	350	355 360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
	365	370 375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
	380	385 390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
	395	400 405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
	410	415 420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
	425	430 435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys
	440	445 450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys
	455	460 465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr
	470	475 480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu
	485	490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

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aacaccctaa tggctggtat atctggatcc tctgctgct ggttttgggtg 250
gcagctcttc tctgtggagc tgtggctctc tgcctccagt gctggctgag 300
gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttggg ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
atgttttggc ccttttaggt cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttggg aaaaattttg gtcattggag tgtttaaata gtaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaacca 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
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tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100
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ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
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ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10					15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 391
cttttcagtgcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 392
ccaaaacatg gagcaggaac agg 23

<210> 393
<211> 47
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 393
 ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 394
 gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
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 gacgcagctg acgcccgcct attagctctc gctgcgtcgc cccggctcag 150
 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
 ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
 cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
 ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
 gtctgtttgt ttgcttcttc agaaatgttt ttacaatct caagaaaaaa 450
 tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatgtggg 500
 gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
 tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650
 tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
 attttgcaac gattggtgaa gctgggagaa aaagttgact atattgttgt 750
 gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtgc 800
 cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850
 ttgaaaatca ccttggtgctg ctccatccac tgtggattat atcctatggc 900
 agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
 aagctctaca catTTTcaag gagtatgctg gattcatgga actctaattc 1000
 tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050
 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggg 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca cttttattta 1200
agtatataac acgttttttg gacaagtga gaatgtttta tcattctgtc 1250
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tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
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catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta atttatgcc attgccagg 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcggccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50
 tccagccccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccggggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ctttctcccc ctttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
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ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
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ttcgagacct ctggaagctt agggcacatt ggttcagcc tagccagttt 2000
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tccccctgag catcctctag atgtgcccc aaggagttgc tgcagttctg 2100

<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
95 100 105
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
110 115 120
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
125 130 135
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
 155 160 165
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
 170 175 180
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
 320 325 330
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
 350

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga agggtagact acgttggctt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat tccccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

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tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggtatTTaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

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tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacgggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
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tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
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ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgacc cttggtcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
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Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
65 70 75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcg cgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttgacca gaatgtgaat gtattgactg gagtggagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
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accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcattg 350
ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
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tgcacttata ttttttagca ctctgatcta caaatttggga agaaccgaag 600
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 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
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 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
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 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
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 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
 80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
 95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
 110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
 125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
 140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
 155

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgctg cagggcagga 50
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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ctttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc ttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcaagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatattga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
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accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 421
 gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1528
 <223> unknown base

<400> 422
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
 tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
 cagcccagga gctcgtctgc tctctctctc tctctctcac tctccctcc 200
 ctctctctct gctgttcta gtctcttagt cctcaaattc ccagtcccct 250
 gcaccccttc ctgggacact atgttggttct ccgccctcct gctggagggtg 300
 atttggatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc 350
 acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
 cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
 ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
 ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
 tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
 cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
 tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
 atgacagctt gaggtaggct gctgagaggc ctcagggcct ggctgtcctg 750
 ggcacccctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

80	85	90
Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 cccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
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 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
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cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtta atcctgccac ccagggaacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
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cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

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<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
95 100 105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
110 115 120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
125 130 135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
140 145 150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
155 160 165

Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
170 175 180

Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
185 190 195

Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
200 205

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
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cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggtccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgctctt gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggagggtgt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
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attgaagcta taattttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
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ttattatgcc ttggaatggt tcacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatggtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
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acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
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tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgagggtgga ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
caggactgag cgcttggtta 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
ccctagctga ccccttca 18

<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
tctgacaagc agttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
ctctccccct cccttttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

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